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RESEARCH NOTE

Genetic analysis of epicuticular wax (bloom) locus in sorghum

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The inheritance pattern of epicuticular wax (bloom) locus in F_1 and F_2 generations of seven sorghum crosses involving a bloomless mutant, RS647 and bloom sorghum parents was studied during the post-rainy season of 2012-13. The plants were scored for bloom and bloomless expression at boot leaf stage. The study revealed that the five crosses BTx623 x RS647, 27A x RS647, 296A x RS647, RS647 x Swathi and IS22380 x RS647 segregated in 3 (bloom) :1 (bloomless) indicating the monogenic control of bloom locus in these crosses. The F_2 of the cross Phule Maulee x RS647 showed a di-genic ratio of 13 (bloom):3 (bloomless) while RS647 x M35-1 cross segregated with 9 (bloom):7 (bloomless) di-genic ratio. The study indicated that the bloom expression is under the control of 1-2 genes based on the genetic background of the parents.

Key words : Epicuticular wax (bloom), Inheritance, Sorghum

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Sorghum (*Sorghum bicolor* L.) is one of the most drought tolerant and water-use efficient cereal crop (Burow *et al.*, 2008). One of the key features that contribute to sorghum drought tolerance is the resence of epicuticular wax (called as “bloom”) on the aerial parts of the plant (Jenks *et al.*,1994). Bloom expression though starts at the seedling stage, its highest expression is generally observed at the boot-leaf stage on the leaves, leaf sheath, peduncle and abaxial side of the leaf blade (Jordan *et al.*,1983 and Jenks *et al.*, 1994 and 2000). Sorghum produces higher amounts of bloom on culms and leaves than other cereals like rice and corn, both on per area and weight bases (Burow *et al.*, 2008; Beattie and Marceil, 2002 and O'Toole and Cruz, 1983). Outer most bloom layer acts as a barrier between the plant and the environment by defending the plant against biotic and abiotic stresses (Blum, 1975 and Jenks and Ashworth, 1999). Most importantly, it restricts the non-stomatal water loss, protects plants against ultraviolet radiation and reduces water retention on the plant surface, thus, minimizing deposition of dust, pollen and air pollutants (Kunst and Samuels, 2003).

Earlier studies in sorghum have indicated the involvement of 1-2 genes in the expression of bloom (Ayyangar and Ponnaiya, 1941; Burow *et al.*, 2008 and Peterson *et al.*, 1982), with bloomless being recessive to both heavy bloom and sparse-bloom. Bloom in sorghum offers green bug resistance (Weibel and Starks, 1986), improved forage digestibility (Cummins and Sudweeks, 1976) and enhanced water use efficiency by regulating night-time water loss (Burow *et al.*, 2008 and Premachandra *et al.*, 1994). In the present study, the inheritance of bloom expression in a series of genetic crosses to understand its genetic control in the background

Table 1: Segregation ratios for bloom (B) and bloomless (BL) plants in F_2 population

Sr.No.	Cross	F_1 Phenotype	No. of F_2 plants	Segregation in F_2		Ratio	χ^2 value	P value
1.	BTx623 x RS647	Bloom	164	128	36	3:1	0.81	0.184
2.	27A x RS647	Bloom	202	153	49	3:1	0.059	0.404
3.	296A x RS647	Bloom	240	171	69	3:1	1.8	0.09
4.	RS647 x Swathi	Bloom	146	113	33	3:1	0.45	0.252
5.	IS22380 x RS647	Bloom	85	67	18	3:1	0.66	0.208
6.	Phule Maulee x RS647	Bloom	141	118	23	13:3	0.55	0.229
7.	RS647 x M35-1	Bloom	146	92	54	9:7	2.71	0.05

of varied genotypes has been reported.

The study involved a bloomless mutant line, RS647 and seven bloom parents, BTx623, 296A, 27A, M35-1, Swathi, Phule Maulee and IS22380. The bloomless mutant, RS647 was developed at the Indian Institute of Millets Research, Rajendranagar, Hyderabad by crossing a Cameroon landrace, IS15703 with an Indian restorer line, RS29. BTx623 is a widely adapted seed parent extensively used in genetic studies and for genome sequencing of sorghum. The lines, 296A and 27A are popular male sterile lines adapted to rainy season while the lines M35-1, Swathi and Phule Maulee are adapted to post-rainy sorghum. IS22380 is a germplasm line from Sudan. Seven F_1s were developed by crossing the bloomless parent, RS647 with seven bloom parents during post-rainy season of 2011. F_1 were grown during the rainy season of 2012 and were selfed to produce the F_2 seed. Seven F_2 populations were raised separately in the experimental fields of IIMR, Hyderabad during the post-rainy season of 2012-13. Plants were grown as a single plant per hill with a spacing of 15 cm between plants and 60 cm between rows. Recommended agronomic practices were followed to raise good crop. Each F_2 plant was labeled. At the boot leaf stage of each F_2 plant, the data on bloom expression was recorded on a binary scale. A plant with bloom was scored as “B” (Bloom) phenotype while those showing the absence of bloom were categorized as “BL” (Bloomless). The goodness of fit between the observed and expected segregation for dominance was responsible for the expression of bloom trait in these crosses. On the other hand, the F_2 plants of cross Phule Maulee x RS647, segregated with a good fit for 13 (bloom):3 (bloomless) suggesting digenic inheritance. Thus, the parents Phule Maulee and RS647 differed for two genes with dominant suppression epistasis in the control of bloom trait. Though the other cross, RS647 x M35-1 also showed involvement of two genes in the development of bloom, but the gene action was complementary with 9 (bloom) : 7 (bloomless) ratio (Table 1). Thus, the expression in sorghum based on the genetic makeup of the parents.

Presently, we are undertaking the genetic mapping of bloom locus to know its location in the sorghum genome. A recent study in sorghum (Burow *et al.*, 2009) mapped a gene for epicuticular wax to chromosome 10, which also showed a monogenic inheritance when crossed with BTx623, one of the parent in the present study. It would be interesting to know whether the same gene is involved in the expression of bloom in the present set of parents involving a different bloomless donor, RS647. Sorghum cuticular wax mutants should provide a valuable resource to elucidate gene involvement in the biosynthesis of cuticular waxes. The genetic mapping of bloom locus with closely linked markers leads to the positional cloning of the gene for its functional analysis to know its role in wax biosynthesis pathway and its role in biotic and abiotic stress tolerance. Development of isogenic lines provides an excellent opportunity to undertake such studies.

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